



SEQUENCE LISTING

(1) GENERAL INFORMATION

(i) APPLICANT: Linsley, Peter S.
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(ii) TITLE OF THE INVENTION: CTLA4/CD28Ig HYBRID FUSION PROTEINS AND USES THEREOF

(iii) NUMBER OF SEQUENCES: 22

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(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Diskette
(B) COMPUTER: IBM Compatible
(C) OPERATING SYSTEM: DOS
(D) SOFTWARE: FastSEQ Version 2.0

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: 09/454,651
(B) FILING DATE: 06-DEC-1999
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 08/228,208
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(B) FILING DATE: 22-JAN-1993

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(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 39 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CTAGCCACTG AAGCTTCACC ATGGGTGTAC TGCTCACAC

39

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 39 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

TGGCATGGGC TCCTGATCAG GCTTAGAAGG TCCGGGAAA

39

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 39 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

TTTGGGCTCC TGATCAGGAA AATGCTCTTG CTTGGTTGT

39

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 84 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

AAGCAAGAGC ATTTCTGA TCAGGAGCCC AAATCTTCTG ACAAAACCTCA CACATCCCCA

60

CCGTCCCCAG CACCTGAACCT CCTG

84

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 41 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CTTCGACCAAG TCTAGAAGCA TCCTCGTGCG ACCGCGAGAG C

41

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 47 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

CATTGCACAG TCAAGCTTCC ATGCCCATGG GTTCTCTGGC CACCTTG

47

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 39 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

ATCCACAGTG CAGTGATCAT TTGGATCCTG GCATGTGAC

39

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 65 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

CTCAGTCTGG TCCTTGCCT CCTGTTCCA AGCATGGCGA GCATGGCAAT GCACGTGGCC

60

CAGCC

65

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 33 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

TTTGGGCTCC TGATCAGAAT CTGGGCACGG TTG

33

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 72 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

CTAGCCACTG AAGCTTCACC AATGGGTGTA CTGCTCACAC AGAGGACGCT GCTCAGTCTG 60

GTCCTTGCAC TC 72

- (2) INFORMATION FOR SEQ ID NO:11:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 33 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GCAATGCACG TGGCCCAGCC TGCTGTGGTA GTG 33

- (2) INFORMATION FOR SEQ ID NO:12:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 45 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

TGATGTAACA TGTCTAGATC AATTGATGGG AATAAAATAA GGCTG 45

- (2) INFORMATION FOR SEQ ID NO:13:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 561 nucleotides
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..561
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GCA ATG CAC GTG GCC CAG CCT GCT GTG GTA CTG GCC AGC AGC CGA GGC 48
 Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg Gly
 1 5 10 15

ATC GCC AGC TTT GTG TGT GAG TAT GCA TCT CCA GGC AAA GCC ACT GAG 96
 Ile Ala Ser Phe Val Cys Glu Tyr Ala Ser Pro Gly Lys Ala Thr Glu
 20 25 30

GTC CGG GTG ACA GTG CTT CGG CAG GCT GAC AGC CAG GTG ACT GAA GTC Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu Val	35	40	45	144	
TGT GCG GCA ACC TAC ATG ATG GGG AAT GAG TTG ACC TTC CTA GAT GAT Cys Ala Ala Thr Tyr Met Met Gly Asn Glu Leu Thr Phe Leu Asp Asp	50	55	60	192	
TCC ATC TGC ACG GGC ACC TCC AGT GGA AAT CAA GTG AAC CTC ACT ATC Ser Ile Cys Thr Gly Thr Ser Ser Gly Asn Gln Val Asn Leu Thr Ile	65	70	75	80	240
CAA GGA CTG AGG GCC ATG GAC ACG GGA CTC TAC ATC TGC AAG GTG GAG Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val Glu	85	90	95	288	
CTC ATG TAC CCA CCG CCA TAC TAC CTG GGC ATA GGC AAC GGA ACC CAG Leu Met Tyr Pro Pro Pro Tyr Tyr Leu Gly Ile Gly Asn Gly Thr Gln	100	105	110	336	
ATT TAT GTA ATT GAT CCA GAA CCG TGC CCA GAT TCT GAC TTC CTC CTC Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp Phe Leu Leu	115	120	125	384	
TGG ATC CTT GCA GCA GTT AGT TCG GGG TTG TTT TTT TAT AGC TTT CTC Trp Ile Leu Ala Ala Val Ser Ser Gly Leu Phe Phe Tyr Ser Phe Leu	130	135	140	432	
CTC ACA GCT GTT TCT TTG AGC AAA ATG CTA AAG AAA AGA AGC CCT CTT Leu Thr Ala Val Ser Leu Ser Lys Met Leu Lys Lys Arg Ser Pro Leu	145	150	155	160	480
ACA ACA GGG GTC TAT GTG AAA ATG CCC CCA ACA GAG CCA GAA TGT GAA Thr Thr Gly Val Tyr Val Lys Met Pro Pro Thr Glu Pro Glu Cys Glu	165	170	175	528	
AAG CAA TTT CAG CCT TAT TTT ATT CCC ATC AAT Lys Gln Phe Gln Pro Tyr Phe Ile Pro Ile Asn	180	185		561	

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 187 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg Gly	1	5	10	15
Ile Ala Ser Phe Val Cys Glu Tyr Ala Ser Pro Gly Lys Ala Thr Glu	20	25	30	
Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu Val				

35	40	45
Cys Ala Ala Thr Tyr Met Met Gly Asn Glu Leu Thr Phe Leu Asp Asp		
50	55	60
Ser Ile Cys Thr Gly Thr Ser Ser Gly Asn Gln Val Asn Leu Thr Ile		
65	70	75
Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val Glu		
85	90	95
Leu Met Tyr Pro Pro Pro Tyr Tyr Leu Gly Ile Gly Asn Gly Thr Gln		
100	105	110
Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp Phe Leu Leu		
115	120	125
Trp Ile Leu Ala Ala Val Ser Ser Gly Leu Phe Phe Tyr Ser Phe Leu		
130	135	140
Leu Thr Ala Val Ser Leu Ser Lys Met Leu Lys Lys Arg Ser Pro Leu		
145	150	155
Thr Thr Gly Val Tyr Val Lys Met Pro Pro Thr Glu Pro Glu Cys Glu		
165	170	175
Lys Gln Phe Gln Pro Tyr Phe Ile Pro Ile Asn		
180	185	

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

AATACGACTC ACTATAGG

18

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

CACCACACTG TATTAACC

18

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 223 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Met Ala Cys Leu Gly Phe Gln Arg His Lys Ala Gln Leu Asn Leu Ala
1 5 10 15
Ala Arg Thr Trp Pro Cys Thr Leu Leu Phe Phe Leu Leu Phe Ile Pro
20 25 30
Val Phe Cys Lys Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala
35 40 45
Ser Ser Arg Gly Ile Ala Ser Phe Val Cys Glu Tyr Ala Ser Pro Gly
50 55 60
Lys Ala Thr Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln
65 70 75 80
Val Thr Glu Val Cys Ala Ala Thr Tyr Met Met Gly Asn Glu Leu Thr
85 90 95
Phe Leu Asp Asp Ser Ile Cys Thr Gly Thr Ser Ser Gly Asn Gln Val
100 105 110
Asn Leu Thr Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile
115 120 125
Cys Lys Val Glu Leu Met Tyr Pro Pro Pro Tyr Tyr Leu Gly Ile Gly
130 135 140
Asn Gly Thr Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser
145 150 155 160
Asp Phe Leu Leu Trp Ile Leu Ala Ala Val Ser Ser Gly Leu Phe Phe
165 170 175
Tyr Ser Phe Leu Leu Thr Ala Val Ser Leu Ser Lys Met Leu Lys Lys
180 185 190
Arg Ser Pro Leu Thr Thr Gly Val Tyr Val Lys Met Pro Pro Thr Glu
195 200 205
Pro Glu Cys Glu Lys Gln Phe Gln Pro Tyr Phe Ile Pro Ile Asn
210 215 220

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 223 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Met Ala Cys Leu Gly Leu Arg Arg Tyr Lys Ala Gln Leu Gln Leu Pro
1 5 10 15
Ser Arg Thr Trp Pro Phe Val Ala Leu Leu Thr Leu Leu Phe Ile Pro
20 25 30
Val Phe Ser Glu Ala Ile Gln Val Thr Gln Pro Ser Val Tyr Leu Ala
35 40 45

Ser Ser His Gly Tyr Ala Ser Phe Pro Cys Glu Tyr Ser Pro Ser His
 50 55 60
 Asn Thr Asp Glu Val Arg Val Thr Val Leu Arg Gln Thr Asn Asp Gln
 65 70 75 80
 Met Thr Glu Val Cys Ala Thr Thr Phe Thr Glu Lys Asn Thr Val Gly
 85 90 95
 Phe Leu Asp Tyr Pro Phe Cys Ser Gly Thr Phe Asn Glu Ser Arg Val
 100 105 110
 Asn Leu Thr Ile Gln Gly Leu Arg Ala Val Asp Thr Gly Leu Tyr Leu
 115 120 125
 Cys Lys Val Glu Leu Met Tyr Pro Pro Pro Tyr Phe Val Gly Met Gly
 130 135 140
 Asn Gly Thr Gln Ile Tyr Tyr Ile Asp Pro Glu Pro Cys Pro Asp Ser
 145 150 155 160
 Asp Phe Leu Leu Trp Ile Leu Tyr Ala Val Ser Leu Gly Leu Phe Phe
 165 170 175
 Tyr Ser Phe Leu Val Ser Ala Val Ser Leu Ser Lys Met Leu Lys Lys
 180 185 190
 Arg Ser Pro Leu Thr Thr Gly Val Tyr Val Lys Met Pro Pro Thr Glu
 195 200 205
 Pro Glu Cys Glu Lys Gln Phe Gln Pro Tyr Phe Ile Pro Ile Asn
 210 215 220

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 218 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Met Thr Leu Arg Leu Leu Phe Leu Ala Leu Asn Phe Phe Ser Val Gln
 1 5 10 15
 Val Thr Glu Asn Lys Ile Leu Val Lys Gln Ser Pro Leu Leu Tyr Val
 20 25 30
 Asp Ser Asn Glu Val Ser Leu Ser Cys Arg Tyr Ser Tyr Asn Leu Leu
 35 40 45
 Ala Lys Glu Phe Arg Ala Ser Leu Tyr Lys Gly Val Asn Ser Asp Val
 50 55 60
 Glu Val Cys Val Gly Asn Gly Asn Phe Thr Tyr Gln Pro Gln Phe Arg
 65 70 75 80
 Ser Asn Ala Glu Phe Asn Cys Asp Gly Asp Phe Asp Asn Glu Thr Val
 85 90 95
 Thr Phe Arg Leu Trp Asn Leu His Val Asn His Thr Asp Ile Tyr Phe
 100 105 110
 Cys Lys Ile Glu Phe Met Tyr Pro Pro Pro Tyr Leu Asp Asn Glu Arg
 115 120 125
 Ser Asn Gly Thr Ile Ile His Ile Lys Glu Lys His Leu Cys His Thr
 130 135 140
 Gln Ser Ser Pro Lys Leu Phe Trp Ala Leu Tyr Val Val Ala Gly Val
 145 150 155 160
 Leu Phe Cys Tyr Gly Leu Leu Val Thr Val Ala Leu Cys Val Ile Trp
 165 170 175

Thr Asn Ser Arg Arg Asn Arg Leu Leu Gln Val Thr Tyr Met Asn Met		
180	185	190
Thr Pro Arg Arg Pro Gly Leu Thr Arg Lys Pro Tyr Gln Pro Tyr Ala		
195	200	205
Pro Ala Arg Asp Phe Ala Ala Tyr Arg Pro		
210	215	

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 218 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Met Thr Leu Arg Leu Leu Phe Leu Ala Leu Ser Phe Phe Ser Val Gln			
1	5	10	15
Val Thr Glu Asn Lys Ile Leu Val Lys Gln Ser Pro Leu Leu Val Tyr			
20	25	30	
Asp Asn Asn Glu Val Ser Leu Ser Cys Arg Tyr Ser Tyr Asn Leu Leu			
35	40	45	
Ala Lys Glu Phe Arg Ala Ser Leu Tyr Lys Gly Val Asn Ser Asp Val			
50	55	60	
Glu Val Cys Val Gly Asn Gly Asn Phe Thr Tyr Gln Pro Gln Phe Arg			
65	70	75	80
Pro Asn Val Gly Phe Asn Cys Asp Gly Asn Phe Asp Asn Glu Thr Val			
85	90	95	
Thr Phe Arg Leu Trp Asn Leu Asp Val Asn His Thr Asp Ile Tyr Phe			
100	105	110	
Cys Lys Ile Glu Val Met Tyr Pro Pro Tyr Leu Asp Asn Glu Lys			
115	120	125	
Ser Asn Gly Thr Ile Ile His Ile Lys Glu Lys His Leu Cys His Ala			
130	135	140	
Gln Thr Ser Pro Lys Leu Phe Trp Pro Leu Val Val Val Ala Gly Val			
145	150	155	160
Leu Leu Cys Tyr Gly Leu Leu Tyr Thr Val Thr Leu Cys Ile Ile Trp			
165	170	175	
Thr Asn Ser Arg Arg Asn Arg Leu Leu Gln Ser Asp Tyr Met Asn Met			
180	185	190	
Thr Pro Arg Arg Leu Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala			
195	200	205	
Pro Ala Arg Asp Phe Ala Ala Tyr Arg Pro			
210	215		

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 220 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Met Leu Arg Leu Leu Ala Leu Asn Leu Phe Pro Ser Ile Gln Val
1 5 10 15
Thr Gly Asn Lys Ile Leu Val Lys Gln Ser Pro Met Leu Val Ala Tyr
20 25 30
Asp Asn Ala Tyr Asn Leu Ser Cys Lys Tyr Ser Tyr Asn Leu Phe Ser
35 40 45
Arg Glu Phe Arg Ala Ser Leu His Lys Gly Leu Asp Ser Ala Val Glu
50 55 60
Val Cys Val Val Tyr Gly Asn Tyr Ser Gln Gln Leu Gln Val Tyr Ser
65 70 75 80
Lys Thr Gly Phe Asn Cys Asp Gly Lys Leu Gly Asn Glu Ser Val Thr
85 90 95
Phe Tyr Leu Gln Asn Leu Tyr Val Asn Gln Thr Asp Ile Tyr Phe Cys
100 105 110
Lys Ile Glu Val Met Tyr Pro Pro Tyr Leu Asp Asn Glu Lys Ser
115 120 125
Asn Gly Thr Ile Ile His Val Lys Gly Lys His Leu Cys Pro Ser Pro
130 135 140
Leu Phe Pro Gly Pro Ser Lys Pro Phe Trp Val Leu Val Val Val Gly
145 150 155 160
Gly Val Leu Ala Cys Tyr Ser Leu Leu Tyr Thr Val Ala Phe Ile Ile
165 170 175
Phe Trp Val Arg Ser Lys Arg Ser Arg Leu Leu His Ser Asp Tyr Met
180 185 190
Asn Met Thr Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro
195 200 205
Tyr Ala Pro Pro Arg Asp Phe Ala Ala Tyr Arg Ser
210 215 220

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 221 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Met Leu Gly Ile Leu Val Val Leu Cys Leu Ile Pro Ala Ala Asp Val
1 5 10 15
Thr Glu Asn Lys Ile Leu Val Ala Gln Arg Pro Leu Leu Ile Val Ala
20 25 30
Asn Arg Thr Ala Thr Leu Val Cys Asn Tyr Thr Tyr Asn Gly Thr Gly
35 40 45
Lys Glu Phe Arg Ala Ser Leu His Lys Gly Thr Asp Ser Ala Val Glu
50 55 60
Val Cys Phe Ile Ser Trp Asn Met Thr Lys Ile Asn Ser Asn Ser Asn
65 70 75 80
Lys Glu Phe Asn Cys Arg Gly Ile His Asp Lys Asp Lys Val Ile Phe
85 90 95

Asn Leu Trp Asn Met Ser Ala Ser Gln Thr Asp Ile Tyr Phe Cys Lys
100 105 110
Ile Glu Ala Met Tyr Pro Pro Pro Tyr Val Tyr Asn Glu Lys Ser Asn
115 120 125
Gly Thr Val Ile His Tyr Arg Glu Thr Pro Ile Gln Thr Gln Glu Pro
130 135 140
Glu Ser Ala Thr Ser Tyr Trp Val Met Tyr Ala Val Thr Gly Leu Leu
145 150 155 160
Gly Phe Tyr Ser Met Leu Ile Thr Ala Val Phe Ile Ile Tyr Arg Gln
165 170 175
Lys Ser Lys Arg Asn Arg Tyr Arg Gln Ser Asp Tyr Met Asn Met Thr
180 185 190
Pro Arg His Pro Pro His Gln Lys Asn Lys Gly Tyr Pro Ser Tyr Ala
195 200 205
Pro Thr Arg Asp Tyr Thr Ala Tyr Arg Ser Trp Gln Pro
210 215 220